



SEQUENCE LISTING

<110> Wolfman, Neil
Bouxsein, Mary

<120> ActRIIB Fusion Polypeptides and Uses Therefor

<130> 08702.0093-000000

<140> US 10/689,677

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<151> 2002-10-25

<160> 6

<170> PatentIn version 3.1

<210> 1

<211> 512

<212> PRT

<213> Human

<400> 1

Met Thr Ala Pro Trp Val Ala Leu Ala Leu Leu Trp Gly Ser Leu Cys
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Ala Gly Ser Gly Arg Gly Glu Ala Glu Thr Arg Glu Cys Ile Tyr Tyr
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Asn Ala Asn Trp Glu Leu Glu Arg Thr Asn Gln Ser Gly Leu Glu Arg
35 40 45

Cys Glu Gly Glu Gln Asp Lys Arg Leu His Cys Tyr Ala Ser Trp Ala
50 55 60

Asn Ser Ser Gly Thr Ile Glu Leu Val Lys Lys Gly Cys Trp Leu Asp
65 70 75 80

Asp Phe Asn Cys Tyr Asp Arg Gln Glu Cys Val Ala Thr Glu Glu Asn
85 90 95

Pro Gln Val Tyr Phe Cys Cys Cys Glu Gly Asn Phe Cys Asn Glu Arg
100 105 110

Phe Thr His Leu Pro Glu Ala Gly Gly Pro Glu Val Thr Tyr Glu Pro
115 120 125

Pro Pro Thr Ala Pro Thr Leu Leu Thr Val Leu Ala Tyr Ser Leu Leu
 130 135 140

Pro Ile Gly Gly Leu Ser Leu Ile Val Leu Leu Ala Phe Trp Met Tyr
 145 150 155 160

Arg His Arg Lys Pro Pro Tyr Gly His Val Asp Ile His Glu Asp Pro
 165 170 175

Gly Pro Pro Pro Pro Ser Pro Leu Val Gly Leu Lys Pro Leu Gln Leu
 180 185 190

Leu Glu Ile Lys Ala Arg Gly Arg Phe Gly Cys Val Trp Lys Ala Gln
 195 200 205

Leu Met Asn Asp Phe Val Ala Val Lys Ile Phe Pro Leu Gln Asp Lys
 210 215 220

Gln Ser Trp Gln Ser Glu Arg Glu Ile Phe Ser Thr Pro Gly Met Lys
 225 230 235 240

His Glu Asn Leu Leu Gln Phe Ile Ala Ala Glu Lys Arg Gly Ser Asn
 245 250 255

Leu Glu Val Glu Leu Trp Leu Ile Thr Ala Phe His Asp Lys Gly Ser
 260 265 270

Leu Thr Asp Tyr Leu Lys Gly Asn Ile Ile Thr Trp Asn Glu Leu Cys
 275 280 285

His Val Ala Glu Thr Met Ser Arg Gly Leu Ser Tyr Leu His Glu Asp
 290 295 300

Val Pro Trp Cys Arg Gly Glu Gly His Lys Pro Ser Ile Ala His Arg
 305 310 315 320

Asp Phe Lys Ser Lys Asn Val Leu Leu Lys Ser Asp Leu Thr Ala Val
 325 330 335

Leu Ala Asp Phe Gly Leu Ala Val Arg Phe Glu Pro Gly Lys Pro Pro
 340 345 350

Gly Asp Thr His Gly Gln Val Gly Thr Arg Arg Tyr Met Ala Pro Glu
355 360 365

Val Leu Glu Gly Ala Ile Asn Phe Gln Arg Asp Ala Phe Leu Arg Ile
370 375 380

Asp Met Tyr Ala Met Gly Leu Val Leu Trp Glu Leu Val Ser Arg Cys
385 390 395 400

Lys Ala Ala Asp Gly Pro Val Asp Glu Tyr Met Leu Pro Phe Glu Glu
405 410 415

Glu Ile Gly Gln His Pro Ser Leu Glu Glu Leu Gln Glu Val Val Val
420 425 430

His Lys Lys Met Arg Pro Thr Ile Lys Asp His Trp Leu Lys His Pro
435 440 445

Gly Leu Ala Gln Leu Cys Val Thr Ile Glu Glu Cys Trp Asp His Asp
450 455 460

Ala Glu Ala Arg Leu Ser Ala Gly Cys Val Glu Glu Arg Val Ser Leu
465 470 475 480

Ile Arg Arg Ser Val Asn Gly Thr Thr Ser Asp Cys Leu Val Ser Leu
485 490 495

Val Thr Ser Val Thr Asn Val Asp Leu Pro Pro Lys Glu Ser Ser Ile
500 505 510

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<211> 375
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<213> Human

<400> 2

Met Gln Lys Leu Gln Leu Cys Val Tyr Ile Tyr Leu Phe Met Leu Ile
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Val Ala Gly Pro Val Asp Leu Asn Glu Asn Ser Glu Gln Lys Glu Asn
20 25 30

Val Glu Lys Glu Gly Leu Cys Asn Ala Cys Thr Trp Arg Gln Asn Thr
35 40 45

Lys Ser Ser Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu
50 55 60

Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Val Ile Arg Gln Leu
65 70 75 80

Leu Pro Lys Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp Val
85 90 95

Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His
100 105 110

Ala Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Phe Leu
115 120 125

Met Gln Val Asp Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser
130 135 140

Lys Ile Gln Tyr Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr Leu
145 150 155 160

Arg Pro Val Glu Thr Pro Thr Thr Val Phe Val Gln Ile Leu Arg Leu
165 170 175

Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu
180 185 190

Lys Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val
195 200 205

Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly
210 215 220

Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val Thr
225 230 235 240

Phe Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val Lys
245 250 255

Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys
260 265 270

Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val
 275 280 285

Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr
 290 295 300

Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys
 305 310 315 320

Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala
 325 330 335

Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr
 340 345 350

Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met Val
 355 360 365

Val Asp Arg Cys Gly Cys Ser
 370 375

<210> 3
 <211> 378
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Chimera/Fusion

<400> 3

Met Lys Phe Leu Val Asn Val Ala Leu Val Phe Met Val Val Tyr Ile
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Ser Tyr Ile Tyr Ala Thr Ser Gly Arg Gly Glu Ala Glu Thr Arg Glu
 20 25 30

Cys Ile Tyr Tyr Asn Ala Asn Trp Glu Leu Glu Arg Thr Asn Gln Ser
 35 40 45

Gly Leu Glu Arg Cys Glu Gly Glu Gln Asp Lys Arg Leu His Cys Tyr
 50 55 60

Ala Ser Trp Arg Asn Ser Ser Gly Thr Ile Glu Leu Val Lys Lys Gly
 65 70 75 80

Cys Trp Leu Asp Asp Phe Asn Cys Tyr Asp Arg Gln Glu Cys Val Ala
85 90 95

Thr Glu Glu Asn Pro Gln Val Tyr Phe Cys Cys Cys Glu Gly Asn Phe
100 105 110

Cys Asn Glu Arg Phe Thr His Leu Pro Glu Ala Gly Gly Pro Glu Val
115 120 125

Thr Tyr Glu Pro Pro Pro Thr Ala Pro Thr Gly Gly Arg Gly Asp Asp
130 135 140

Asp Asp Lys Thr Arg Ser Arg Asp Lys Thr His Thr Cys Pro Pro Cys
145 150 155 160

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
165 170 175

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
180 185 190

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
195 200 205

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
210 215 220

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
225 230 235 240

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
245 250 255

Lys Ala Leu Pro Val Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
260 265 270

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
275 280 285

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
290 295 300

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
 305 310 315 320

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
 325 330 335

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
 340 345 350

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
 355 360 365

Gln Lys Ser Leu Ser Leu Ser Pro Pro Lys
 370 375

<210> 4
 <211> 1134
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Chimera/Fusion

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 gagctggagc gcaccaacca gagcggcctg gagcgctgcg aaggcgagca ggacaagcgg 180
 ctgcactgct acgcctcctg gcgcaacagc tctggcacca tcgagctcgt gaagaagggc 240
 tgctggctag atgacttcaa ctgctacgat aggcaggagt gtgtggccac tgaggagaac 300
 ccccagggtg acttctgctg ctgtgaaggc aacttctgca acgagcgctt cactcatttg 360
 ccagaggctg ggggcccgga agtcacgtac gagccacccc cgacagcccc caccggcggc 420
 cgcgagagcg acgacgacaa gacgcgttct agagacaaaa ctcacacatg cccaccgtgc 480
 ccagcacctg aactcctggg gggaccgtca gtcttctct tcccccaaa acccaaggac 540
 accctcatga tctcccggac ccctgaggtc acatgcgtgg tggaggacgt gagccacgaa 600
 gaccctgagg tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca 660
 aagccgcggg aggagcagta caacagcacg taccgtgtgg tcagcgtcct caccgtcctg 720
 caccaggact ggctgaatgg caaggagtac aagtgcgaagg tctccaacaa agccctccca 780
 gtcccatcg agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac 840

accctgcccc catcccgga ggagatgacc aagaaccagg tcagcctgac ctgcctggtc 900
aaaggcttct atcccagcga catcgccgtg gaggggaga gcaatgggca gccggagaac 960
aactacaaga ccacgcctcc cgtgctggac tccgacggct ccttcttct ctatagcaag 1020
ctcaccgtgg acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat 1080
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<210> 5
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Linking Sequence, Gly-Ser repeat

<400> 5

Gly Ser Gly Ser
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<210> 6
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Linking Sequence, Enterokinase Cleavage Site

<400> 6

Asp Asp Asp Lys
1